Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Original) A method of conducting a (*N*,*N*-*K*) dimensional (D) G-matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiment, wherein *N* is the dimensionality of an *N*-dimensional (*N*D) Fourier transformation (FT) NMR experiment and *K* is the desired reduction in dimensionality relative to *N*, said method comprising:

providing a sample;

applying radiofrequency pulses for the *N*D FT NMR experiment to the sample;

selecting *m* indirect chemical shift evolution periods of the *N*D FT NMR experiment, wherein *m* equals *K*+1;

jointly sampling the *m* indirect chemical shift evolution periods;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate (*N*-*K*)D basic NMR spectra comprising frequency domain signals with 2^K chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled *m* indirect chemical shift evolution periods; and

transforming the (*N*-*K*) D basic NMR spectra into (*N*-*K*) D phase-sensitively edited basic NMR spectra, wherein the 2^K chemical shift multiplet components of the (*N*-*K*) D basic NMR spectra are edited to yield (*N*-*K*) D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

2. (Original) The method according to claim 1, wherein said transforming is carried out by applying a G-matrix defined as $\hat{G}(K) = \left[\begin{bmatrix} 1 & i \\ 1 & -i \end{bmatrix} \otimes \ldots \otimes \begin{bmatrix} 1 & i \\ 1 & -i \end{bmatrix} \otimes \begin{bmatrix} 1 & i \end{bmatrix}\right]$, wherein $i = \sqrt{-1}$, under conditions effective to edit the chemical shift multiplet components in a time domain.

3. (Original) The method according to claim 1, wherein said transforming is carried out by applying a F-matrix defined as $\hat{F}(K) = \hat{F}(K-1) \otimes \hat{F}(1)$, wherein $\hat{F}(1) = \begin{bmatrix} 1 & 1 \\ 1 & -1 \end{bmatrix}$, under conditions effective to edit the chemical shift multiplet components in a frequency domain.

4. (Original) The method according to claim 1 further comprising:

selecting *m*' indirect chemical shift evolution periods of the (*N-K*)D FT NMR experiment, wherein *m*' equals *K*'+1;

jointly sampling the *m*' indirect chemical shift evolution periods;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate (*N-K-K*')D basic NMR spectra comprising frequency domain signals with $2^{K'}$ chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled *m*' indirect chemical shift evolution periods; and

transforming the (*N-K-K*') D basic NMR spectra into (*N-K-K*') D phase-sensitively edited basic NMR spectra, wherein the $2^{K'}$ chemical shift multiplet components of the (*N-K-K*') D basic NMR spectra are edited to yield (*N-K-K*') D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

5. (Original) The method according to claim 4 further comprising:

repeating one or more times said selecting, said jointly sampling, said independently cosine and sine modulating, and said transforming, wherein *m*' is modified for each repetition.

6. (Original) The method according to claim 1 further comprising:

repeating one or more times said selecting, said jointly sampling, said independently cosine and sine modulating, and said transforming, wherein, for each repetition, said selecting comprises selecting *m-j* indirect chemical shift evolution periods out of the *m* indirect chemical shift evolution periods, wherein *j* ranges from 1 to *K*, under conditions effective to generate 2^{K-j} *j*th order central peak NMR spectra.

7. (Original) The method according to claim 1, wherein said applying radiofrequency pulses is carried out by applying radiofrequency pulses of *N*-dimensional nuclear Overhauser enhancement spectroscopy (NOESY).

8. (Original) The method according to claim 1, wherein said applying radiofrequency pulses is carried out by applying radiofrequency pulses of *N*-dimensional transverse relaxation optimized spectroscopy (TROSY).

9. (Original) The method according to claim 1, wherein said applying radiofrequency pulses is carried out so that spin-spin couplings are measured.

10. (Original) The method according to claim 9, wherein said spin-spin couplings are residual dipolar spin-spin coupling constants.

11. (Original) The method according to claim 1, wherein said jointly sampling the *m* indirect chemical shift evolution periods is achieved with a single continuous acquisition.

12. (Original) The method according to claim 1, wherein said applying radiofrequency pulses is carried out so that nuclear spin relaxation times are measured by sampling nuclear spin relaxation delays.

13. (Original) The method according to claim 12 further comprising:

jointly sampling said spin relaxation delays with chemical shift evolution periods.

14. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [<u>HACACON</u>HN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, *i*-1 and *i*, and the chemical shift values for the following nuclei are measured: (1) an α-proton of amino acid residue *i*-1, $^{1}H^{\alpha}_{i-1}$; (2) an α-carbon of amino acid residue *i*-1, $^{13}C^{\alpha}_{i-1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$; (4) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_{i}$; and (5) a polypeptide backbone amide proton of amino acid residue *i*,

${}^{1}\mathrm{H}^{\mathrm{N}}{}_{i}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, ${}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}$, ${}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}$, ${}^{13}\mathrm{C'}_{i\text{-}1}$, and ${}^{15}\mathrm{N}_{i}$, and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1({}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}, {}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}, {}^{13}\mathrm{C'}_{i\text{-}1}, {}^{15}\mathrm{N}_{i})$.

15. (Original) The method according to claim 14, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 5D FT NMR experiment according to the scheme shown in Figure 6.

16. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [HACA,CONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, and the chemical shift values for the following nuclei are measured: (1) an α-proton of amino acid residue *i*-1, ${}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}$; (2) an α-carbon of amino acid residue *i*-1, ${}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, ${}^{13}\mathrm{C'}_{i\text{-}1}$; (4) a polypeptide backbone amide nitrogen of amino acid residue *i*-1, ${}^{15}\mathrm{N}_{i\text{-}1}$; and (5) a polypeptide backbone amide proton of amino acid residue *i*-1, ${}^{1}\mathrm{H}^{\mathrm{N}}{}_{i\text{-}1}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, ${}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}$, ${}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}$, ${}^{13}\mathrm{C'}_{i\text{-}1}$, and ${}^{15}\mathrm{N}_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1({}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}, {}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}, {}^{13}\mathrm{C'}_{i\text{-}1}, {}^{15}\mathrm{N}_{i\text{-}1})$.

17. (Original) The method according to claim 16, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 5D FT NMR experiment according to the scheme shown in Figure 7A.

18. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [HACACONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, *i*-1 and *i*, and the chemical shift values for the following nuclei are measured: (1) an α-proton of amino acid residue *i*-1, ${}^{1}\mathrm{H}^{\alpha}{}_{i\text{-}1}$; (2) an α-carbon of amino acid residue *i*-1, ${}^{13}\mathrm{C}^{\alpha}{}_{i\text{-}1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, ${}^{13}\mathrm{C'}_{i\text{-}1}$; (4) a polypeptide backbone amide nitrogen of amino

acid residue i, $^{15}N_i$; and (5) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\alpha}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha}_{i\text{-}1}, {}^{13}C^{\alpha}_{i\text{-}1}, {}^{13}C'_{i\text{-}1})$.

19. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [<u>HACA,CO</u>NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having an amino acid residue, i-1, and the chemical shift values for the following nuclei are measured: (1) an α-proton of amino acid residue i-1, $^{1}H^{\alpha}_{i\text{-}1}$; (2) an α-carbon of amino acid residue i-1, $^{13}C^{\alpha}_{i\text{-}1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i\text{-}1}$; (4) a polypeptide backbone amide nitrogen of amino acid residue i-1, $^{15}N_{i\text{-}1}$; and (5) a polypeptide backbone amide proton of amino acid residue i-1, $^{1}H^{N}_{i\text{-}1}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\alpha}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha}_{i\text{-}1}, {}^{13}C^{\alpha}_{i\text{-}1}, {}^{13}C'_{i\text{-}1})$.

20. (Original) The method according to claim 1, wherein N equals 4 and K equals 1 to conduct a (4,3)D [<u>CBCACO</u>NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i\text{-}1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i\text{-}1}$ and $^{13}C'_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i\text{-}1}, {}^{13}C'_{i\text{-}1})$.

21. (Original) The method according to claim 20, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 8.

22. (Original) The method according to claim 1, wherein N equals 4 and K equals 1 to conduct a (4,3)D [CBCA,CONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having an amino acid residue, *i*-1, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i-1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue *i*-1, $^{15}N_{i-1}$; and (4) a polypeptide backbone amide proton of amino acid residue *i*-1, $^{1}H^{N}_{i-1}$, (b) said selecting comprises selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i-1}$ and $^{13}C'_{i-1}$, and (c) said jointly sampling comprises jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i-1}, {}^{13}C'_{i-1})$.

23. (Original) The method according to claim 22, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 7B.

24. (Original) The method according to claim 1, wherein N equals 4 and K equals 1 to conduct a (4,3)D [HNNCACBCA] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, *i*-1 and *i*, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residues *i* and *i*-1, $^{13}C^{\alpha/\beta}_{i/i-1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_{i}$; and (3) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i/i-1}$ and $^{13}C^{\alpha}_{i/i-1}$, and (c) said jointly sampling comprises jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i/i-1}, {}^{13}C^{\alpha}_{i/i-1})$.

25. (Original) The method according to claim 24, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 9.

26. (Original) The method according to claim 1, wherein N equals 4 and K equals 2 to conduct a (4,2)D [HNNCACBCA] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residues i and i-1, $^{13}C^{\alpha/\beta}_{i/i-1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (3) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i/i-1}$, $^{13}C^{\alpha}_{i/i-1}$, and $^{15}N_i$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i/i-1}, {}^{13}C^{\alpha}_{i/i-1}, {}^{15}N_i)$.

27. (Original) The method according to claim 1, wherein N equals 4 and K equals 1 to conduct a (4,3)D [HNN(CO)CACBCA] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (3) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$, and (c) said jointly sampling comprises jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i-1}, {}^{13}C^{\alpha}_{i-1})$.

28. (Original) The method according to claim 27, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 10.

29. (Original) The method according to claim 1, wherein N equals 4 and K equals 2 to conduct a (4,2)D [HNN(CO)CACBCA] GFT NMR experiment, wherein (a) said sample is

a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i-1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (3) a polypeptide backbone amide proton of amino acid residue i, $^1H^N{}_i$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i-1}$, $^{13}C^{\alpha}{}_{i-1}$, and $^{15}N_i$; and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i-1}, ^{13}C^{\alpha}{}_{i-1}, ^{15}N_i)$.

30. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [HNNCOCACBCA] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i-1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, (3) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue i, $^1H^N{}_i$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i-1}$, $^{13}C^{\alpha}{}_{i-1}$, and $^{13}C'_{i-1}$, (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i-1}, ^{13}C^{\alpha}{}_{i-1}, ^{13}C'_{i-1})$.

31. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [HNNCOCACBCA] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i-1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, (3) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue i, $^1H^N{}_i$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i-1}$, $^{13}C^{\alpha}{}_{i-1}$, $^{13}C'_{i-1}$, and $^{15}N_i$; and (c) said jointly sampling comprises jointly sampling the

4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i\text{-}1}, {}^{13}C^{\alpha}{}_{i\text{-}1}, {}^{13}C'_{i\text{-}1}, {}^{15}N_i)$.

32. (Original) The method according to claim 1, wherein N equals 4 and K equals 1 to conduct a (4,3)D [CBCACA(CO)NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i\text{-}1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (3) a polypeptide backbone amide proton of amino acid residue i, $^1H^N{}_i$, (b) said selecting comprises selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i\text{-}1}$ and $^{13}C^{\alpha}{}_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i\text{-}1}, {}^{13}C^{\alpha}{}_{i\text{-}1})$.

33. (Original) The method according to claim 32, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 11.

34. (Original) The method according to claim 1, wherein N equals 4 and K equals 2 to conduct a (4,2)D [CBCACA(CO)NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i\text{-}1}$; (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (3) a polypeptide backbone amide proton of amino acid residue i, $^1H^N{}_i$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i\text{-}1}$, $^{13}C^{\alpha}{}_{i\text{-}1}$, and $^{15}N_i$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i\text{-}1}, {}^{13}C^{\alpha}{}_{i\text{-}1}, {}^{15}N_i)$.

35. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [CBCACACONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, i-1 and i, and the chemical

shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i\text{-}1}$, (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$, (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i\text{-}1}, ^{13}C^{\alpha}_{i\text{-}1}, ^{13}C'_{i\text{-}1})$.

36. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [CBCACACONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two consecutive amino acid residues, *i*-1 and *i*, and the chemical shift values for the following nuclei are measured: (1) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$; (2) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i\text{-}1}$, (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, $^{13}C^{\alpha/\beta}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, $^{13}C'_{i\text{-}1}$, and $^{15}N_i$; (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}_{i\text{-}1}, ^{13}C^{\alpha}_{i\text{-}1}, ^{13}C'_{i\text{-}1}, ^{15}N_i)$.

37. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two amino acid residues, *i* and *i*-1, and the chemical shift values for the following nuclei are measured: (1) α- and β- protons of amino acid residue *i*-1, $^{1}H^{\alpha/\beta}_{i\text{-}1}$; (2) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\alpha/\beta}_{i\text{-}1}$, $^{13}C^{\alpha/\beta}_{i\text{-}1}$, and $^{13}C^{\alpha}_{i\text{-}1}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha/\beta}_{i\text{-}1}, ^{13}C^{\alpha/\beta}_{i\text{-}1}, ^{13}C^{\alpha}_{i\text{-}1})$.

38. (Original) The method according to claim 37, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 5D FT NMR experiment according to the scheme shown in Figure 12.

39. (Original) The method according to claim 1, wherein N equals 6 and K equals 3 to conduct a (6,3)D [HBHACBCACACONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two amino acid residues, *i* and *i*-1, and the chemical shift values for the following nuclei are measured: (1) α- and β protons of amino acid residue *i*-1, $^{1}H^{\alpha/\beta}_{i-1}$; (2) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i-1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$; (4) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (5) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 6D FT NMR experiment, $^{1}H^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, and $^{13}C'_{i-1}$, and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha/\beta}_{i-1}, {}^{13}C^{\alpha/\beta}_{i-1}, {}^{13}C^{\alpha}_{i-1}, {}^{13}C'_{i-1})$.

40. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [HBHACBCACA(CO)NHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two amino acid residues, *i* and *i*-1, and the chemical shift values for the following nuclei are measured: (1) α- and β protons of amino acid residue *i*-1, $^{1}H^{\alpha/\beta}_{i-1}$; (2) α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i-1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, and $^{15}N_i$, and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha/\beta}_{i-1}, {}^{13}C^{\alpha/\beta}_{i-1}, {}^{13}C^{\alpha}_{i-1}, {}^{15}N_i)$.

41. (Original) The method according to claim 1, wherein N equals 6 and K equals 4 to conduct a (6,2)D [HBHACBCACACONHN] GFT NMR experiment, wherein (a) said sample is a protein molecule having two amino acid residues, *i* and *i*-1, and the chemical shift

values for the following nuclei are measured: (1) α- and β protons of amino acid residue i-1, $^{1}H^{\alpha/\beta}_{i-1}$; (2) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$; (3) a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$; (4) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$; and (5) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$, (b) said selecting comprises selecting 5 chemical shift evolution periods of the 6D FT NMR experiment, $^{1}H^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, $^{13}C'_{i-1}$, and $^{15}N_i$, and (c) said jointly sampling comprises jointly sampling the 5 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\alpha/\beta}_{i-1}, ^{13}C^{\alpha/\beta}_{i-1}, ^{13}C^{\alpha}_{i-1}, ^{13}C'_{i-1}, ^{15}N_i)$.

42. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [HCC,CH-COSY] GFT NMR experiment, wherein (a) the chemical shift values for the following nuclei are measured: (1) a proton, ^{1}H; (2) a carbon coupled to ^{1}H, ^{13}C; and (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$; and (4) a proton coupled to $^{13}C^{coupled}$, $^{1}H^{coupled}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, ^{1}H, ^{13}C, and $^{13}C^{coupled}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H, ^{13}C, ^{13}C^{coupled})$.

43. (Original) The method according to claim 42, wherein said chemical shift evolution periods for ^{13}C and $^{13}C^{coupled}$ are correlated using total correlation spectroscopy (TOCSY).

44. (Original) The method according to claim 42, wherein (a) said sample is a protein molecule having an amino acid residue, i, and the chemical shift values for the following nuclei are measured: (1) a proton of amino acid residue i, $^{1}H_i$; (2) a carbon of amino acid residue i coupled to $^{1}H_i$, $^{13}C_i$; and (3) a carbon coupled to $^{13}C_i$, $^{13}C_i^{coupled}$; and (4) a proton coupled with $^{13}C_i^{coupled}$, $^{1}H_i^{coupled}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H_i$, $^{13}C_i$, and $^{13}C_i^{coupled}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H_i, ^{13}C_i, ^{13}C_i^{coupled})$.

45. (Original) The method according to claim 44, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 5D FT NMR experiment according to the scheme shown in Figure 13.

46. (Original) The method according to claim 1, wherein N equals 5 and K equals 2 to conduct a (5,3)D [HBCBCGCDHD] GFT NMR experiment, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, with an aromatic side chain, and the chemical shift values for the following nuclei are measured: (1) a β–proton of amino acid residue *i*, $^1H^{\beta}_{i}$; (2) a β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$; (3) a γ-carbon of amino acid residue *i*, $^{13}C^{\gamma}_{i}$; (4) a δ-carbon of amino acid residue *i*, $^{13}C^{\delta}_{i}$; and (5) a δ–proton of amino acid residue *i*, $^1H^{\delta}_{i}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^1H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, and $^{13}C^{\delta}_{i}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H^{\beta}_{i},{}^{13}C^{\beta}_{i},{}^{13}C^{\delta}_{i})$.

47. (Original) The method according to claim 46, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 5D FT NMR experiment according to the scheme shown in Figure 14.

48. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [HBCBCGCDHD] GFT NMR experiment, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, with an aromatic side chain, and the chemical shift values for the following nuclei are measured: (1) a β–proton of amino acid residue *i*, $^1H^{\beta}_{i}$; (2) a β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$; (3) a γ-carbon of amino acid residue *i*; (4) a δ-carbon of amino acid residue *i*, $^{13}C^{\delta}_{i}$; and (5) a δ–proton of amino acid residue *i*, $^1H^{\delta}_{i}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, $^1H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{13}C^{\gamma}_{i}$, and $^{13}C^{\delta}_{i}$, and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H^{\beta}_{i},{}^{13}C^{\beta}_{i},{}^{13}C^{\gamma}_{i},{}^{13}C^{\delta}_{i})$.

49. (Original) The method according to claim 1, wherein N equals 4 and K equals 2 to conduct a (4,2)D [HCCH-COSY] GFT NMR experiment, wherein (a) the chemical shift values for the following nuclei are measured: (1) a proton, ^{1}H; (2) a carbon coupled to ^{1}H, ^{13}C; (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$; and (4) a proton coupled to $^{13}C^{coupled}$, $^{1}H^{coupled}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, ^{1}H, ^{13}C, and $^{13}C^{coupled}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H,^{13}C,^{13}C^{coupled})$.

50. (Original) The method according to claim 49, wherein said chemical shift evolution periods for ^{13}C and $^{13}C^{coupled}$ are correlated using total correlation spectroscopy (TOCSY).

51. (Original) The method according to claim 49, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, and the chemical shift values for the following nuclei are measured: (1) a proton of amino acid residue *i*, $^{1}H_i$; (2) a carbon of amino acid residue *i* coupled to $^{1}H_i$, $^{13}C_i$; (3) a carbon coupled to $^{13}C_i$, $^{13}C_i^{coupled}$; and (4) a proton coupled to $^{13}C_i^{coupled}$, $^{1}H_i^{coupled}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, $^{1}H_i$, $^{13}C_i$, and $^{13}C_i^{coupled}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H_i,^{13}C_i,^{13}C_i^{coupled})$.

52. (Original) The method according to claim 51, wherein said applying radiofrequency pulses comprises applying radiofrequency pulses for a 4D FT NMR experiment according to the scheme shown in Figure 15.

53. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,2)D [HCCCH-COSY] GFT NMR experiment, wherein (a) the chemical shift values for the following nuclei are measured: (1) a proton ^{1}H; (2) a carbon coupled to ^{1}H, ^{13}C; (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$; (4) a carbon coupled to $^{13}C^{coupled}$, $^{13}C^{coupled\text{-}2}$; and (5) a proton coupled with $^{13}C^{coupled\text{-}2}$, $^{1}H^{coupled\text{-}2}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, ^{1}H, ^{13}C, $^{13}C^{coupled}$, and $^{13}C^{coupled\text{-}2}$,and

(c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H,^{13}C,^{13}C^{coupled},^{13}C^{coupled\text{-}2})$.

54. (Original) The method according to claim 53, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, and the chemical shift values for the following nuclei are measured: (1) a proton of amino acid residue *i*, ^1H_i; (2) a carbon of amino acid residue *i* coupled to ^1H_i, $^{13}C_i$; (3) a carbon coupled to $^{13}C_i$, $^{13}C_i^{coupled}$; (4) a carbon coupled to $^{13}C_i^{coupled}$, $^{13}C_i^{coupled\text{-}2}$; and (5) a proton coupled with $^{13}C_i^{coupled\text{-}2}$, $^1H_i^{coupled\text{-}2}$, (b) said selecting comprises selecting 4 chemical shift evolution periods of the 5D FT NMR experiment, ^1H_i, $^{13}C_i$, $^{13}C_i^{coupled}$, and $^{13}C_i^{coupled\text{-}2}$,and (c) said jointly sampling comprises jointly sampling the 4 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H_i,^{13}C_i,^{13}C_i^{coupled},^{13}C_i^{coupled\text{-}2})$.

55. (Original) The method according to claim 1, wherein N equals 5 and K equals 3 to conduct a (5,3)D [<u>HCC</u>CH-COSY] GFT NMR experiment, wherein (a) the chemical shift values for the following nuclei are measured: (1) a proton, ^1H; (2) a carbon coupled to ^1H, ^{13}C; (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$; (4) a carbon coupled to $^{13}C^{coupled}$, $^{13}C^{coupled\text{-}2}$; and (5) a proton coupled with $^{13}C^{coupled\text{-}2}$, $^1H^{coupled\text{-}2}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, ^1H, ^{13}C, and $^{13}C^{coupled}$, and (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H,^{13}C,^{13}C^{coupled})$.

56. (Original) The method according to claim 55, wherein (a) said sample is a protein molecule having an amino acid residue, *i*, and the chemical shift values for the following nuclei are measured: (1) a proton of amino acid residue *i*, ^1H_i; (2) a carbon of amino acid residue *i* coupled to ^1H_i, $^{13}C_i$; (3) a carbon coupled to $^{13}C_i$, $^{13}C_i^{coupled}$; (4) a carbon coupled to $^{13}C_i^{coupled}$, $^{13}C_i^{coupled\text{-}2}$; and (5) a proton coupled with $^{13}C_i^{coupled\text{-}2}$, $^1H_i^{coupled\text{-}2}$, (b) said selecting comprises selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, ^1H_i, $^{13}C_i$, and $^{13}C_i^{coupled}$, (c) said jointly sampling comprises jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H_i,^{13}C_i,^{13}C_i^{coupled})$.

57. (Original) A method for sequentially assigning chemical shift values of an α-proton, $^1H^\alpha$, an α-carbon, $^{13}C^\alpha$, a polypeptide backbone carbonyl carbon, $^{13}C'$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^1H^N$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (5,2)D [HACACONHN] GFT NMR experiment to measure and connect the chemical shift values of the α-proton of amino acid residue *i*-1, $^1H^\alpha_{i\text{-}1}$, the α-carbon of amino acid residue *i*-1, $^{13}C^\alpha_{i\text{-}1}$, the polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i\text{-}1}$, the polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue *i*, $^1H^N_i$ and (2) a (5,2)D [HACA,CONHN] GFT NMR experiment to measure and connect the chemical shift values of $^1H^\alpha_{i\text{-}1}$, $^{13}C^\alpha_{i\text{-}1}$, $^{13}C'_{i\text{-}1}$, the polypeptide backbone amide nitrogen of amino acid residue *i*-1, $^{15}N_{i\text{-}1}$, and the polypeptide backbone amide proton of amino acid residue *i*-1, $^1H^N_{i\text{-}1}$; and

obtaining sequential assignments of the chemical shift values of $^1H^\alpha$, $^{13}C^\alpha$, $^{13}C'$, ^{15}N, and $^1H^N$ by (i) matching the chemical shift values of $^1H^\alpha_{i\text{-}1}$, $^{13}C^\alpha_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$ measured by said (5,2)D [HACACONHN] GFT NMR experiment with the chemical shift values of $^1H^\alpha_{i\text{-}1}$, $^{13}C^\alpha_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$ measured by said (5,2)D [HACA,CONHN] GFT NMR experiment, (ii) using the chemical shift values of $^1H^\alpha_{i\text{-}1}$, $^{13}C^\alpha_{i\text{-}1}$, and $^{13}C'_{i\text{-}1}$ to identify the type of amino acid residue *i*-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

58. (Original) The method according to claim 57 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

59. (Original) The method according to claim 57 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

60. (Original) The method according to claim 57 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

61. (Original) A method for sequentially assigning chemical shift values of an α-proton, $^1H^\alpha$, an α-carbon, $^{13}C^\alpha$, a polypeptide backbone carbonyl carbon, $^{13}C'$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^1H^N$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (5,3)D [<u>HACACO</u>NHN] GFT NMR experiment to measure and connect the chemical shift values of the α-proton of amino acid residue *i*-1, $^1H^\alpha_{i-1}$, the α-carbon of amino acid residue *i*-1, $^{13}C^\alpha_{i-1}$, the polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue *i*, $^1H^N_i$ and (2) a (5,3)D [<u>HACA,CO</u>NHN] GFT NMR experiment to measure and connect the chemical shift values of $^1H^\alpha_{i-1}$, $^{13}C^\alpha_{i-1}$, $^{13}C'_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue *i*-1, $^{15}N_{i-1}$, and the polypeptide backbone amide proton of amino acid residue *i*-1, $^1H^N_{i-1}$; and

obtaining sequential assignments of the chemical shift values of $^1H^\alpha$, $^{13}C^\alpha$, $^{13}C'$, ^{15}N, and $^1H^N$ by (i) matching the chemical shift values of $^1H^\alpha_{i-1}$, $^{13}C^\alpha_{i-1}$, and $^{13}C'_{i-1}$ measured by said (5,3)D [<u>HACACO</u>NHN] GFT NMR experiment with the chemical shift values of $^1H^\alpha_{i-1}$, $^{13}C^\alpha_{i-1}$, and $^{13}C'_{i-1}$ measured by said (5,3)D [<u>HACA,CO</u>NHN] GFT NMR experiment, (ii) using the chemical shift values of $^1H^\alpha_{i-1}$, $^{13}C^\alpha_{i-1}$, and $^{13}C'_{i-1}$ to identify the type of amino acid residue *i*-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

62. (Original) The method according to claim 61 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

63. (Original) The method according to claim 61 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

64. (Original) The method according to claim 61 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

65. (Original) A method for sequentially assigning chemical shift values of α- and β-carbons, $^{13}C^{\alpha/\beta}$, a polypeptide backbone carbonyl carbon, $^{13}C'$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (4,3)D [CBCACONHN] GFT NMR experiment to measure and connect the chemical shift values of the α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$, the polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$ and (2) a (4,3)D [CBCA,CONHN] GFT NMR experiment to measure and connect the chemical shift values of $^{13}C^{\alpha/\beta}_{i-1}$, $^{13}C'_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue i-1, $^{15}N_{i-1}$, and the polypeptide backbone amide proton of amino acid residue i-1, $^{1}H^{N}_{i-1}$; and

obtaining sequential assignments of the chemical shift values of $^{13}C^{\alpha/\beta}$, $^{13}C'$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of $^{13}C^{\alpha/\beta}_{i-1}$ and $^{13}C'_{i-1}$ measured by said (4,3)D [CBCACONHN] GFT NMR experiment with the chemical shift values of $^{13}C^{\alpha/\beta}_{i-1}$ and $^{13}C'_{i-1}$ measured by said (4,3)D [CBCA,CONHN] GFT NMR experiment, (ii) using the chemical shift values of $^{13}C^{\alpha/\beta}_{i-1}$ and $^{13}C'_{i-1}$ to identify the type of amino acid residue i-1, and (iii)

mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

66. (Original) The method according to claim 65 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

67. (Original) The method according to claim 65 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

68. (Original) The method according to claim 65 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

69. (Original) A method for sequentially assigning chemical shift values of α- and β-carbons, $^{13}C^{\alpha/\beta}$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (4,3)D [HNN<u>CACBCA</u>] GFT NMR experiment to measure and connect the chemical shift values of the α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$, the α-carbon of amino acid residue i-1, $^{13}C^{\alpha}_{i\text{-}1}$, the polypeptide backbone amide nitrogen of amino acid residue i-1, $^{15}N_{i\text{-}1}$, and the polypeptide backbone amide proton of amino acid residue i-1, $^{1}H^{N}_{i\text{-}1}$ and (2) a GFT NMR experiment selected from the group consisting of a (4,3)D [HNN(CO)<u>CACBCA</u>] GFT NMR experiment, a (4,3)D [<u>CBCACA</u>(CO)NHN] GFT NMR experiment , and a (5,3)D [<u>HBHACBCACA</u>(CO)NHN] GFT NMR experiment to measure and connect the chemical shift values of $^{13}C^{\alpha/\beta}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, the polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_{i}$, and the polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{13}C^{\alpha/\beta}$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of $^{13}C^{\alpha/\beta}{}_{i-1}$ measured by said GFT NMR experiment selected from the group consisting of a (4,3)D [HNN(CO)CACBCA] GFT NMR experiment, a (4,3)D [CBCACA(CO)NHN] GFT NMR experiment , and a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment with the chemical shift values of $^{13}C^{\alpha/\beta}{}_{i-1}$ measured by said (4,3)D [HNNCACBCA] GFT NMR experiment, (ii) using the chemical shift values of $^{13}C^{\alpha/\beta}{}_{i-1}$ to identify the type of amino acid residue i-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

70. (Original) The method according to claim 69 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

71. (Original) The method according to claim 69 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

72. (Original) The method according to claim 69 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

73. (Original) A method for assigning chemical shift values of γ-, δ-, and ε-aliphatic sidechain protons, $^{1}H^{\gamma/\delta/\varepsilon}$, and chemical shift values of γ-, δ-, and ε-aliphatic sidechain carbons located peripheral to β-carbons, $^{13}C^{\gamma/\delta/\varepsilon}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (5,3)D [HCC,CH-COSY] GFT NMR experiment to measure and connect the chemical shift values of a proton of amino acid residue i-1, $^{1}H_{i-1}$, a carbon of amino acid residue i-1 coupled to $^{1}H_{i-1}$, $^{13}C_{i-1}$, a

carbon coupled to $^{13}C_{i\text{-}1}$, $^{13}C_{i\text{-}1}^{coupled}$, and a proton coupled to $^{13}C_{i\text{-}1}^{coupled}$, $^{1}H_{i\text{-}1}^{coupled}$, and (2) a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment to measure and connect the chemical shift values of α- and β-protons of amino acid residue *i*-1, $^{1}H^{\alpha/\beta}_{i\text{-}1}$, and α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i\text{-}1}$; and

obtaining assignments of the chemical shift values of $^{1}H^{\gamma/\delta/\varepsilon}$ and $^{13}C^{\gamma/\delta/\varepsilon}$ by (i) identifying $^{1}H_{i\text{-}1}$, $^{13}C_{i\text{-}1}$, $^{13}C_{i\text{-}1}^{coupled}$, and $^{1}H_{i\text{-}1}^{coupled}$ measured by said (5,3)D [HCC,CH-COSY] GFT NMR experiment as $^{1}H^{\alpha}_{i\text{-}1}$, $^{13}C^{\alpha}_{i\text{-}1}$, $^{13}C^{\beta}_{i\text{-}1}$, and $^{1}H^{\beta}_{i\text{-}1}$, respectively, and thereby matching the chemical shift values of $^{1}H^{\alpha/\beta}_{i\text{-}1}$ and $^{13}C^{\alpha/\beta}_{i\text{-}1}$ with the chemical shift values of $^{1}H^{\alpha/\beta}_{i\text{-}1}$ and $^{13}C^{\alpha/\beta}_{i\text{-}1}$ measured by said (5,3)D HBHACBCACA(CO)NHN] GFT NMR experiment, and (ii) using the chemical shift values of $^{1}H^{\alpha/\beta}_{i\text{-}1}$ and $^{13}C^{\alpha/\beta}_{i\text{-}1}$ in conjunction with other chemical shift connections from said (5,3)D [HCC,CH-COSY] GFT NMR experiment to measure the chemical shift values of $^{1}H^{\gamma/\delta/\varepsilon}_{i\text{-}1}$ and $^{13}C^{\gamma/\delta/\varepsilon}_{i\text{-}1}$.

74. (Original) The method according to claim 73 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

75. (Original) The method according to claim 73 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

76. (Original) The method according to claim 73 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

77. (Original) A method for assigning chemical shift values of γ-, δ-, and ε-aliphatic sidechain protons, $^{1}H^{\gamma/\delta/\varepsilon}$, and chemical shift values of γ-, δ-, and ε-aliphatic sidechain carbons located peripheral to β-carbons, $^{13}C^{\gamma/\delta/\varepsilon}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (4,2)D [HCCH-

COSY] GFT NMR experiment to measure and connect the chemical shift values of a proton of amino acid residue i-1, $^{1}H_{i-1}$, a carbon of amino acid residue i-1 coupled to $^{1}H_{i-1}$, $^{13}C_{i-1}$, a carbon coupled to $^{13}C_{i-1}$, $^{13}C_{i-1}^{coupled}$, and a proton coupled to $^{13}C_{i-1}^{coupled}$, $^{1}H_{i-1}^{coupled}$, and (2) a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment to measure and connect the chemical shift values of α- and β-protons of amino acid residue i-1, $^{1}H^{\alpha/\beta}_{i-1}$, and α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$; and

obtaining assignments of the chemical shift values of $^{1}H^{\gamma/\delta/\varepsilon}$ and $^{13}C^{\gamma/\delta/\varepsilon}$ by (i) identifying $^{1}H_{i-1}$, $^{13}C_{i-1}$, $^{13}C_{i-1}^{coupled}$, and $^{1}H_{i-1}^{coupled}$ measured by said (4,2)D [HCCH-COSY] GFT NMR experiment as $^{1}H^{\alpha}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, $^{13}C^{\beta}_{i-1}$, and $^{1}H^{\beta}_{i-1}$, respectively, and thereby matching the chemical shift values of $^{1}H^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha/\beta}_{i-1}$ with the chemical shift values of $^{1}H^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha/\beta}_{i-1}$ measured by said (5,3)D HBHACBCACA(CO)NHN] GFT NMR experiment, and (ii) using the chemical shift values of $^{1}H^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha/\beta}_{i-1}$ in conjunction with other chemical shift connections from said (4,2)D [HCCH-COSY] GFT NMR experiment to measure the chemical shift values of $^{1}H^{\gamma/\delta/\varepsilon}_{i-1}$ and $^{13}C^{\gamma/\delta/\varepsilon}_{i-1}$.

78. (Original) The method according to claim 77 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

79. (Original) The method according to claim 77 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

80. (Original) The method according to claim 77 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

81. (Original) A method for assigning chemical shift values of a γ-carbon, $^{13}C^{\gamma}$, a δ-carbon, $^{13}C^{\delta}$, and a δ-proton, $^{1}H^{\delta}$, of an amino acid residue containing an aromatic spin system in a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a (5,3)D [HBCBCGCDHD] GFT NMR experiment to measure and connect the chemical shift values of a β-proton of amino acid residue i-1, $^1H^{\beta}_{i-1}$, a β-carbon of amino acid residue i-1, $^{13}C^{\beta}_{i-1}$, a γ-carbon of amino acid residue i-1, $^{13}C^{\gamma}_{i-1}$, a δ-carbon of amino acid residue i-1, $^{13}C^{\delta}_{i-1}$, and a δ-proton of amino acid residue i-1, $^1H^{\delta}_{i-1}$, and (2) a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment to measure and connect the chemical shift values of $^1H^{\beta}_{i-1}$ and $^{13}C^{\beta}_{i-1}$; and

obtaining assignments of the chemical shift values of $^{13}C^{\gamma}$, $^{13}C^{\delta}$, and $^1H^{\delta}$ by (i) matching the chemical shift values of $^1H^{\beta}_{i-1}$ and $^{13}C^{\beta}_{i-1}$ measured by said (5,3)D HBCBCACA(CO)NHN GFT NMR experiment with the chemical shift values of $^1H^{\beta}_{i-1}$ and $^{13}C^{\beta}_{i-1}$ measured by said (5,3)D [HBCBCGCDHD] GFT NMR experiment, and (ii) using the chemical shift values of $^{13}C^{\gamma}$, $^{13}C^{\delta}$, and $^1H^{\delta}$ to identify the type of amino acid residue containing the aromatic spin system.

82. (Original) The method according to claim 81 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

83. (Original) The method according to claim 81 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

84. (Original) The method according to claim 81 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

85. (Original) A method for assigning chemical shift values of aliphatic and aromatic protons and aliphatic and aromatic carbons of an amino acid residue containing aliphatic and aromatic spin systems in a protein molecule comprising:

providing a protein sample;

conducting a set of G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a first GFT NMR experiment, which is selected from the group consisting of a (5,3)D [<u>HCC</u>,CH-COSY] GFT NMR experiment, a (4,2)D [<u>HCC</u>H-COSY] GFT NMR experiment, a (5,2)D [<u>HCCC</u>H-COSY] GFT NMR experiment, and a (5,3)D [<u>HCC</u>CH-COSY] GFT NMR experiment and is acquired for the aliphatic spin system, to measure and connect the chemical shift values of α- and β-protons of amino acid residue *i*, $^1H^{\alpha/\beta}{}_i$, α- and β-carbons of amino acid residue *i*, $^{13}C^{\alpha/\beta}{}_i$, a γ-carbon of amino acid residue *i*, $^{13}C^{\gamma}{}_i$, and (2) a second GFT NMR experiment, which is selected from the group consisting of a (5,3)D [<u>HCC</u>,CH-COSY] GFT NMR experiment, a (4,2)D [<u>HCC</u>H-COSY] GFT NMR experiment, a (5,2)D [<u>HCCC</u>H-COSY] GFT NMR experiment, and a (5,3)D [<u>HCC</u>CH-COSY] GFT NMR experiment and is acquired for the aromatic spin system, to measure and connect the chemical shift values of $^{13}C^{\gamma}{}_i$ and other aromatic protons and carbons of amino acid residue *i*; and

obtaining assignments of the chemical shift values of the aliphatic and aromatic protons and aliphatic and aromatic carbons by matching the chemical shift value of $^{13}C^{\gamma}{}_i$ measured by said first GFT NMR experiment with the chemical shift value of $^{13}C^{\gamma}{}_i$ measured by said second GFT NMR experiment.

86. (Original) The method according to claim 85, wherein said conducting a set of GFT NMR experiments is carried out by using $^{13}C^{\gamma}$ steady state magnetization to generate first order central peaks.

87. (Original) The method according to claim 85 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

88. (Original) The method according to claim 85 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

89. (Original) The method according to claim 85 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

90. (Original) A method for obtaining assignments of chemical shift values of ^{1}H, ^{13}C, and ^{15}N of a protein molecule comprising:

providing a protein sample; and

conducting five G matrix Fourier transformation (GFT) nuclear magnetic resonance (NMR) experiments on the protein sample, wherein (1) a first experiment is a (4,3)D [HNNCACBCA] GFT NMR experiment for obtaining intraresidue correlations of chemical shift values; (2) a second experiment is a (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment for obtaining interresidue correlations of chemical shift values; (3) a third experiment is a (5,3)D [HCC,CH-COSY] GFT NMR experiment for obtaining assignments of aliphatic sidechain chemical shift values; (4) a fourth experiment is a (5,3)D [HBCBCGCDHD] GFT NMR experiment for linking chemical shift values of aliphatic protons, $^{1}H^{\beta}$ and $^{13}C^{\beta}$, and aromatic protons, $^{13}C^{\delta}$ and $^{1}H^{\delta}$; and (5) a fifth experiment is a (4,2)D [HCCH-COSY] GFT NMR experiment for obtaining assignments of aromatic sidechain chemical shift values.

91. (Original) The method according to claim 90 further comprising:

subjecting the protein sample to nuclear Overhauser enhancement spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

92. (Original) The method according to claim 90 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

93. (Original) The method according to claim 90 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.

94. (New) The method according to claim 90, wherein said (4,3)D [HNNCACBCA] GFT NMR experiment is conducted by a method of measuring the

chemical shift values for (1) α- and β-carbons of amino acid residues i and i-1, $^{13}C^{\alpha/\beta}{}_{i/i-1}$, (2) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$, and (3) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}{}_{i}$, of a protein molecule having two consecutive amino acid residues, i-1 and i, said method comprising:

providing a sample;

applying radiofrequency pulses for the 4D FT NMR experiment to the sample;

selecting 2 chemical shift evolution periods of the 4D FT NMR experiment, $^{13}C^{\alpha/\beta}{}_{i/i-1}$ and $^{13}C^{\alpha}{}_{i/i-1}$;

jointly sampling the 2 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{13}C^{\alpha/\beta}{}_{i/i-1}, {}^{13}C^{\alpha}{}_{i/i-1})$;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate 3D basic NMR spectra comprising frequency domain signals with 2 chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled 2 indirect chemical shift evolution periods; and

transforming the 3D basic NMR spectra into 3D phase-sensitively edited basic NMR spectra, wherein the 2 chemical shift multiplet components of the 3D basic NMR spectra are edited to yield 3D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

95. (New) The method according to claim 90, wherein said (5,3)D [HBHACBCACA(CO)NHN] GFT NMR experiment is conducted by a method of measuring the chemical shift values for (1) α- and β- protons of amino acid residue i-1, $^{1}H^{\alpha/\beta}{}_{i-1}$, (2) α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}{}_{i-1}$, (3) a polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$, and (4) a polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}{}_{i}$, of a protein molecule having two amino acid residues, i and i-1, said method comprising:

providing a sample;

applying radiofrequency pulses for the 5D FT NMR experiment to the sample;

selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\alpha/\beta}{}_{i-1}$, $^{13}C^{\alpha/\beta}{}_{i-1}$, and $^{13}C^{\alpha}{}_{i-1}$;

jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H^{\alpha/\beta}{}_{i-1}, {}^{13}C^{\alpha/\beta}{}_{i-1}, {}^{13}C^{\alpha}{}_{i-1})$;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate 3D basic NMR spectra comprising frequency domain signals with 4 chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled 3 indirect chemical shift evolution periods; and

transforming the 3D basic NMR spectra into 3D phase-sensitively edited basic NMR spectra, wherein the 4 chemical shift multiplet components of the 3D basic NMR spectra are edited to yield 3D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

96. (New) The method according to claim 90, wherein said (5,3)D [HCC,CH-COSY] GFT NMR experiment is conducted by a method of measuring the chemical shift values for (1) a proton, ^1H, (2) a carbon coupled to ^1H, ^{13}C, (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$, and (4) a proton coupled to $^{13}C^{coupled}$, $^1H^{coupled}$, of a protein molecule, said method comprising:

providing a sample;

applying radiofrequency pulses for the 5D FT NMR experiment to the sample;

selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, ^1H, ^{13}C, and $^{13}C^{coupled}$;

jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^1H, {}^{13}C, {}^{13}C^{coupled})$;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate 3D basic NMR spectra comprising frequency domain signals with 4 chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled 3 indirect chemical shift evolution periods; and

transforming the 3D basic NMR spectra into 3D phase-sensitively edited basic NMR spectra, wherein the 4 chemical shift multiplet components of the 3D basic NMR spectra are edited to yield 3D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

97. (New) The method according to claim 90, wherein said (5,3)D [HBCBCGCDHD] GFT NMR experiment is conducted by a method of measuring the chemical shift values for (1) a β–proton of amino acid residue i, $^{1}H^{\beta}_{i}$, (2) a β-carbon of amino acid residue i, $^{13}C^{\beta}_{i}$, (3) a γ-carbon of amino acid residue i, $^{13}C^{\gamma}_{i}$, (4) a δ-carbon of amino acid residue i, $^{13}C^{\delta}_{i}$, and (5) a δ–proton of amino acid residue i, $^{1}H^{\delta}_{i}$, of a protein molecule having an amino acid residue, i, with an aromatic side chain, said method comprising:

providing a sample;

applying radiofrequency pulses for the 5D FT NMR experiment to the sample;

selecting 3 chemical shift evolution periods of the 5D FT NMR experiment, $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, and $^{13}C^{\delta}_{i}$;

jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H^{\beta}_{i}, {}^{13}C^{\beta}_{i}, {}^{13}C^{\delta}_{i})$;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate 3D basic NMR spectra comprising frequency domain signals with 4 chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled 3 indirect chemical shift evolution periods; and

transforming the 3D basic NMR spectra into 3D phase-sensitively edited basic NMR spectra, wherein the 4 chemical shift multiplet components of the 3D basic NMR spectra are edited to yield 3D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.

98. (New) The method according to claim 90, wherein said (4,2)D [HCCH-COSY] GFT NMR experiment is conducted by a method of measuring the chemical shift values for (1) a proton, ^{1}H, (2) a carbon coupled to ^{1}H, ^{13}C, (3) a carbon coupled to ^{13}C, $^{13}C^{coupled}$, and (4) a proton coupled to $^{13}C^{coupled}$, $^{1}H^{coupled}$, of a protein molecule, said method comprising:

providing a sample;

applying radiofrequency pulses for the 4D FT NMR experiment to the sample;

selecting 3 chemical shift evolution periods of the 4D FT NMR experiment, ^{1}H, ^{13}C, and $^{13}C^{coupled}$;

jointly sampling the 3 chemical shift evolution periods in an indirect time domain dimension, $t_1(^{1}H,^{13}C,^{13}C^{coupled})$;

independently cosine and sine modulating NMR signals detected in a direct dimension to generate 2D basic NMR spectra comprising frequency domain signals with 4 chemical shift multiplet components, thereby enabling phase-sensitive sampling of all jointly sampled 3 indirect chemical shift evolution periods; and

transforming the 2D basic NMR spectra into 2D phase-sensitively edited basic NMR spectra, wherein the 4 chemical shift multiplet components of the 2D basic NMR spectra are edited to yield 2D phase-sensitively edited basic NMR spectra having individual chemical shift multiplet components.